

IN THE SPECIFICATION:

Please amend page 1, second to the last paragraph as follows:

Searchers seeking the function or characteristics of a particular gene or protein have been so far provided with any of the following methods. In one method, the aforementioned first database is searched using the sequence information of the gene or protein as a search key. An identifier for data in the second database is extracted from the data obtained from the first database, and then the data in the second database is obtained. Referring to that data, the searcher can then learn the function or characteristics of the gene or protein described therein. As an example of this method, a method called BLAST (<http://www.ncbi.nlm.nih.gov/BLAST/>) is widely employed.

Please amend page 4, last paragraph as follows:

Fig. 2 shows the structure of the text data 106 in the first file system 105. In this example, the data is in the form of a thesis describing the result of research into a particular base sequence. The text data 106 includes a base or amino acid sequence 201 (SEQ ID NO: 1) as the subject of description in the data, and an identifier 202 of other text data in which there is description related to the present data. In the illustrated example, there are two items of related text data with respect to the present data, two identifiers are stored. In this example, the identifiers are indicated as PMID (PubMed ID).

Please amend page 7, second to the last paragraph as follows:

In step 802, it is checked to see if all of the sequences (SEQ ID NOs: 2 and 3) entered in the input field 401 of the search start page of Fig. 4 have been processed. If all of the sequences have been processed, the routine proceeds to step 814, and if not, the routine proceeds to step 803.

Please amend page 8, 4th paragraph as follows:

In step 809, the identifier 301 of the present data is taken out from the text data file [[106]]108, and it is then determined whether the identifier 301 corresponds to any of the identifiers 202 of text data files 106 taken out in step 806. If it does, the routine proceeds to step 810, and if not, the routine returns to step 807 where another file is taken out and the subsequent processes are carried out.